



## Protein families database of alignments and HMMs

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ubiquitin



**Figure 1: 1ndd**  
**Signaling protein**  
Structure of nedd8

### Key:

D main	Chain	Start Residue	End Residue
<a href="#">ubiquitin</a>	A	1	74
<a href="#">ubiquitin</a>	B	101	174
<a href="#">ubiquitin</a>	C	201	273
<a href="#">ubiquitin</a>	D	301	373

The Swissprot/PDB mapping was provided by [MSD](#)

1a5r

Display pdb

Accession number: PF00240

### Ubiquitin family

[Add Annotation](#)

This family contains a number of ubiquitin-like proteins: SUMO (smt3 homologue) (see [ULP1\\_YEAST](#)), Nedd8 (see [NED8\\_MOUSE](#)), Elongin B (see [Q15370](#)), Rub1 (see [Q9SHE7](#)).

This family forms **structural complexes** with other Pfam families, to view them click [here](#)

### INTERPRO description (entry IPR000626)

Ubiquitin [[MEDLINE:91274342](#)], PUB00000768, PUB00000768 is a protein of seventy six amino acid residues, found in alleukaryotic cells and whose sequence is extremely well conserved from protozoan to vertebrates. It is widely known as a post-translational tag used to signal a protein's hydrolytic destruction. Other functions for ubiquitin, depend on its differential internal isopeptide linkages. In addition, several ubiquitin-like proteins have been discovered from genome-sequencing efforts, other structural studies, and genetic screens. These new data show that proteins with the ubiquitin domain are adaptable, transposable genetic elements, which have been appended to other genes and utilized for many different cellular functions, depending on the ubiquitin-like protein's identity, subcellular location, and method of covalent attachment. The post-translational ligation of proteins to members of the ubiquitin superfamily can signal many different fates for the target protein [Larsen and Wang (2002) J. Proteome Res. 1, 411-419.]

Ubiquitin is a globular protein, the last four C-terminal residues (Leu-Arg-Gly-Gly) extending from the compact structure to form a 'tail' important for its function. The latter is mediated by the covalent conjugation of ubiquitin to target proteins, by an isopeptide linkage between the C-terminal glycine and the epsilon amino group of lysine residues in the target proteins.

In most species, there are many genes coding for ubiquitin. However they can be classified into two classes. The first class produces polyubiquitin molecules consisting of exact head to tail repeats of ubiquitin. The number of repeats is variable. In the majority of polyubiquitin precursors, there is a final amino-acid after the last repeat. The second class of genes produces precursor proteins consisting of a single copy of ubiquitin fused to a C-terminal extension protein (CEP). There are two types of CEP proteins and both seem to be ribosomal proteins. There are a number of proteins which are evolutionary related to ubiquitin, including ubiquitin-like proteins from baculoviruses; mammalian proteins GDX, FAU and RAD23-related proteins; human spliceosome associated protein 114, proteins BAT3 and CKAP1/TFCB, and ubiquitin-like proteins SMT3A, SMT3C and SMT3B; yeast proteins RAD23, DK2 and SMT3; and *Caenorhabditis elegans* SMT3 and ubl-1 proteins.

For additional annotation, see the [PROSITE](#) document PDOC00271 [[ExPASy](#) | [SRS-UK](#) | [SRS-USA](#)]

Alignment	Domain organisation
<input checked="" type="radio"/> Seed (95) <input type="radio"/> Full (1365) Format <input type="text" value="Coloured alignment"/> <div> <input type="button" value="Get alignment"/> <input type="button" value="View HMM logo"/> </div> Further alignment options here Help relating to Pfam alignments <a href="#">here</a>	<input checked="" type="radio"/> Seed (95) <input type="radio"/> Full (1365) <input type="radio"/> Context (3) <div> <div> <b>As a Graphic</b>            Zoom <input type="text" value="0.5"/> pixels/aa. <input type="checkbox"/> Bootstrap tree  <input type="button" value="View Graphic"/> </div> <div> <b>As a Tree</b>  <input type="button" value="NIFAS Applet"/> </div> </div> To find out about the NIFAS tree-viewer, click <a href="#">here</a>
Species Distribution	Phylogenetic tree
<b>NEW!</b> View alignments & domain organisation by species Tree depth: <input type="text" value="Show all levels"/> <input type="button" value="View Species Tree"/>	<input checked="" type="radio"/> Seed (95) <input type="radio"/> Full (1365) <div> <input type="button" value="Download tree"/> <input type="button" value="ATV Applet"/> </div> The trees were generated using <a href="#">Quicktree</a> To find out more about ATV phylogenetic tree-viewer <a href="#">click here</a>

Database References	
<b>PDB</b> You can find out how to set up Rasmol <a href="#">here</a>	<input type="text" value="1bt0 A; 1; 73;"/> <div> </div>
<b>PROSITE</b>	PDOC00271 [ <a href="#">Expasy</a>   <a href="#">SRS-UK</a>   <a href="#">SRS-USA</a> ]
<b>PRINTS</b>	<a href="#">PR00348</a>
<b>HOMSTRAD</b>	<a href="#">UBQ</a>
<b>PFAMB</b>	<a href="#">PB027829</a> <a href="#">PB039948</a> <a href="#">PB048702</a> <a href="#">PB068927</a> <a href="#">PB083641</a> <a href="#">PB088642</a> <a href="#">PB0927</a> <a href="#">PB096446</a>
<b>SYSTERS</b>	<a href="#">ubiquitin</a>
<b>PANDIT</b>	<a href="#">ubiquitin</a>

Literature References	Pfam specific information	
1. <b>Structure of ubiquitin refined at 1.8 Å resolution.</b> Vijay-Kumar S, Bugg CE, Cook WJ; <i>J Mol Biol</i> 1987;194:531-544.	Author of entry	Finn RD, Griffiths-Jones SR
2. <b>Structure of tetraubiquitin shows how multiubiquitin chains can be formed.</b> Cook WJ, Jeffrey LC, Kasperek E, Pickart CM; <i>J Mol Biol</i> 1994;236:601-609.	Type definition	Domain
3. <b>Structure determination of</b>	Alignment method of seed	Clustalw
	Source of seed members	Prosite
	HMMER build information	
	Pfam_ls [ <a href="#">Download HMM</a> ]	Pfam_fs [ <a href="#">Download HMM</a> ]
	Gathering cutoff	25.5 25.5; 11.2 11.2

<b><u>the small ubiquitin-related modifier SUMO-1.</u></b> Bayer P, Arndt A, Metzger S, Mahajan R, Melchior F, Jaenicke R, Becker J; J Mol Biol 1998;280:275-286.	Trusted cutoff	26.2 26.1;	11.2 11.2
	Noise cutoff	25.2 25.2;	11.1 11.1
	Build method of HMM	hmmbuild -F HMM_Is SEED hmmcalibrate --seed 0 HMM_Is	hmmbuild -f -F HMM_fs SEED hmmcalibrate --seed 0 HMM_fs
<b>4.</b> <b><u>Crystal structure of the human ubiquitin-like protein NEDD8 and interactions with ubiquitin pathway enzymes.</u></b> Whitby FG, Xia G, Pickart CM, Hill CP; J Biol Chem 1998;273:34983-34991.			

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